AMENDMENTS TO THE CLAIMS

1. (**Currently Amended**) [[M]] A method for determining an absolute concentration of one or more mRNA molecules in a sample, comprising ~~mRNA quantities by means of DNA microarrays with the following steps~~:

a. providing a DNA microarray comprising a plurality of immobilized probes and including one or more dilution series of control spots;

b. ~~providing at least one or more dilution series of control spots on the microarray~~ hybridizing the immobilized probes with the sample or cDNA made from the sample;

c. hybridizing the immobilized probes with a corresponding control DNA of known concentration;

d. deriving reference data from ~~the hybridization~~ step c; and

e. using said reference data to calculate absolute mRNA concentrations in said sample ~~one or more samples used~~.

2. (**Currently Amended**) [[M]] The method according to claim 1, further comprising ~~the step of~~ providing a universal tag at each of the immobilized probes on the microarray to be used for quantification.

3. (**Currently Amended**) [[M]] The method according to claim 1 or 2, wherein [[a]] the DNA microarray is a cDNA microarray, ~~and/or~~ the control DNA is control cDNA, or both.

4. (**Currently Amended**) [[M]] The method according to claim 1 or 2 ~~any of the preceding claims~~, wherein the reference data comprise a model curve which is fitted or adapted to ~~the obtained~~ signals obtained from the [[for]] control spots.

5. (**Currently Amended**) [[M]] The method according to claim 1 or 2 ~~any of the preceding claims,~~ wherein cDNA probes ~~templates for the genes that are to be probed for~~ are first amplified by large-scale multiplex polymerase chain reaction (PCR) to obtain amplified fragments prior to immobilization on the DNA microarray.

6. (**Currently Amended**) [[M]] The method according to claim 5, wherein said amplified fragments are then transferred to the microarray by means of robotic ~~roboting~~ devices which are able to deliver nanoliter quantities with a spatial precision of better than 100 μm.

7. (**Currently Amended**) [[M]] The method according to claim 1 or 2 ~~any one of the preceding claims~~, wherein the reference data of step d ~~obtained from the hybridization, e.g., the read-out signal intensities from the dilution series spots,~~ are taken as a basis for calculating [[the]] parameters of a model function by means of non-linear least-squares fitting.

8. (**Currently Amended**) [[M]] The method according to claim 7, wherein for the model function the following function is used:

$$\hat{I} = \frac{KI_0 e^{rc_p}}{K + I_0(e^{rc_p} - 1)}$$

wherein the function has a modeled signal intensity, a probe (or DNA spot) concentration, an asymptotic signal intensity for $c_p \rightarrow \infty$, and an asymptotic signal intensity for $c_p \rightarrow 0$, and where $\hat{I}$ refers to the modeled signal intensity, c_p refers to the probe (or DNA spot) concentration, K represents the asymptotic signal intensity for $c_p \rightarrow \infty$, I_0 is the asymptotic signal intensity for $c_p \rightarrow 0$, and r is a shape parameter.

9. (**Currently Amended**) [[M]] The method according to claim 7 ~~any one of claims 4-8~~, wherein fitting ~~of~~ the reference data is done by gradient optimization procedures.

10. (**Currently Amended**) [[M]] The method according to claim 9, wherein Newton-Raphson fitting is used for non-linear fitting~~, the Newton-Raphson method is used~~.

11. (**Currently Amended**) [[M]] The method according to claim 1 or 2 ~~any one of the preceding claims~~, wherein a critical probe function is used to determine [[the]] a set of spots whose values

need correction for [[the]] influence of spot DNA concentration, wherein a [[the]] critical probe concentration function is [[being]] defined by

$$c_{crit} = \frac{1}{r}\left[\ln\frac{17(K - I_0)}{3I_0}\right].$$

12. (**Currently Amended**) [[C]] A computer program product comprising program code means stored on a computer readable medium for performing [[the]] a computable part of the method of claim 7~~at least one of the preceding claims~~ when said program product is run on a computer.

13. (**Currently Amended**) [[S]] A system~~, particularly~~ for performing the method of claim 1 or 2 ~~at least one of claims 1-11~~, comprising:

a. a microarray containing at least one or more dilution series of control spots;

b. means for hybridizing with a complementary control DNA of known concentration;

c. means for deriving reference data from ~~said hybridization~~ step b, and

d. means for making use of said reference data for calculating absolute mRNA concentrations ~~in one or more samples used~~.

14. (**Currently Amended**) [[S]] A system according to claim 13, further comprising means for providing a universal tag at each of the immobilized probes on the microarray to be used for quantification.

15. (**Currently Amended**) [[Use of a]] A method for determining an absolute quantity of one or more mRNA molecules in a sample, comprising performing the method of claim 7 ~~according to at least one of claims 1-11~~ using a computer to execute a computer program that performs calculations that carry out at least part of the method. ~~product according to claim 12 and/or a system according to at least one of claims 13 or 14 for determining absolute mRNA quantities on cDNA microarrays.~~

16. (**Cancelled**)

17. (**New**) A method for determining an absolute quantity of one or more mRNA molecules in a sample, comprising performing the method of claim 7 using a system comprising:

a. a microarray containing at least one or more dilution series of control spots;

b. means for hybridizing with a complementary control DNA of known concentration;

c. means for deriving reference data from step b, and

d. means for making use of said reference data for calculating absolute mRNA concentrations in one or more samples used.

18. (**New**) A method for determining an absolute concentration of one or more nucleic acid molecules in a sample, comprising:

a. providing a DNA microarray having a plurality of immobilized probes and one or more dilution series of control spots;

b. hybridizing the immobilized probes with the sample or cDNA made from the sample;

c. hybridizing the immobilized probes with a corresponding control nucleic acid of known concentration;

d. deriving reference data from step c; and

e. using said reference data to calculate absolute nucleic acid concentrations in said sample.